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Re: June, 1980 letter proposing a nomenclature for viral onc genes

Dear Harold and John,

Your idea to name retroviral transforming genes is excellent. So are some of the "rules" for the naming game. However, it is obvious to me that few if any retroviral transforming genes are as yet rigorously defined. A helper-virus-unrelated, X- or transformation-specific- or, worst of all, "cellular" sequence is not the same as a viral transforming gene. Nevertheless, I agree that these sequences are at present the most unambiguous candidates for naming with three-letter symbols. As you acknowledge they are only alleles which are part of transforming genes, that have yet to be genetically defined. I am particularly impressed by the rules that names should be trivial and mellifluous and mnemonic.

Since I did not detect much adherence to these rules in the three-letter names proposed in your letter, I thought of an alternate proposal: name the alleles of a given subgroup of transforming viruses (subgroup defined on the basis of a common RNA/DNA sequence) after the first viral prototype in which this sequence was identified. This is in keeping with your, J. M. Bishop's, and our lab's proposals at CSH in 1979. For example the specific sequence of the MC29 subgroup of viruses would be termed mcv, that of Fujinami virus fsv, that of avian erythroblastosis virus aev, that of avian myeloblastosis virus amv, that of Moloney msv, that of Harvey and Kirsten hsv and those of feline sarcoma viruses either stv or sfv for Sneider-Theilen and mdv or mfv for the McDonough strain. Substrains could be identified by additional hyphenated letters as you propose in your letter. This nomenclature meets the crucial rules of being trivial, mnemonic and is also pronounceable and simple to refer to. It certainly provides preferable alternatives to such convoluted structures as fps that nobody will be able to decipher as an acronym or pronounce unless highly familiar with the science, history and politics of the field. The problem with the mac's, myb's, and erb's is simply that these names indicate specificities that are nonexistent. (For example, AEV, E26 and MC29 all cause erythroblastosis in chicken or in addition to myelocytomatosis, MC29 causes sarcomas and carcinomas in chicken and even transforms rat fibroblasts.) Moreover, your triviality rule and Lwoff's and Andrewes' principles of virus classification would all be violated if disease were again used as a basis for virus classification. Therefore I have not and will not use these terms in the future.

Obviously to make this a consistent system, *src* should be called *rsv*. This would be alright with me, although it may be a bit late by now to rename this gene. Moreover the *src* gene unlike most transforming genes is genetically defined and as such more than an allele and may therefore deserve a special place. It is an excellent example to illustrate the problem with naming genes after the disease they cause. Now that the Fujinami virus is analyzed, its *fsv* gene would be as deserving of the name *src* as *src* of RSV.

A last suggestion is to avoid all super- or subscripts in subclassifying genes or gene products. This is particularly funny when it leads to such mellifluous triple deckers as $P115^{gag\text{-}fes^{S}}$. Subclassification should be done by hyphens on the same level.

All the best,

Peter

Peter Duesberg

PD:td

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